

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Presta, Leonard G.  
Shelton, David L.  
Urfer, Roman
- (ii) TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
- (iii) NUMBER OF SEQUENCES: 41
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP  
(B) STREET: 620 Newport Center Drive, 16th Floor  
(C) CITY: Newport Beach  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 92660
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: not yet assigned  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/446172  
(B) FILING DATE: 19-MAY-1995
- (viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/286846  
(B) FILING DATE: 05-AUG-1994
- (xi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/215139  
(B) FILING DATE: 18-MAR-1994
- (x) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Dreger, Ginger  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
- (xi) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 954-4114  
(B) TELEFAX: (415) 954-4111

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3194 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAC CGCAAAGCGC AGGGAAAGGCC TCCCGGCACG 50  
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100  
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150  
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200  
TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250  
CGACCCTTCT CCTGGCATCG TGGCATTCC GAGATTGGAG CCTAACAGTG 300  
TAGATCCTGA GAACATCACCC GAAATTTCA TCGCAAACCA GAAAAGGTTA 350  
GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGAC TGAGAAATCT 400  
GACAATTGTG GATTCTGGAT TAAAATTGT GGCTCATAAA GCATTCTGA 450  
AAAACAGCAA CCTGCAGCAC ATCAATTAA CCCGAAACAA ACTGACGAGT 500  
TTGTCTAGGA AACATTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATAACCA ATTGTGGTT 700  
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900  
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950  
AACCTCACTG TGCATTTGC ACCAACTATC ACATTCTCG AATCTCCAAC 1000

CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050  
CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
CCAGCTGGAT AATCCCAC TC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
CCAAGAACATGA GTATGGGAAG GATGAGAAC AGATTTCTGC TCACTTCATG 1250  
GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
TTATGAAGAT TATGGAAC TG CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTG 1450  
CCTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTG 1500  
GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550  
CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600  
TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650  
ATCCCCAGTA CTTTGGCATH ACCAACAGTC AGCTCAAGCC AGACACATTT 1700  
GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750  
AGGAGCCTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800  
AGCAGGACAA GATCTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850  
AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900  
GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950  
TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCCTC 2000  
AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCCAC 2050  
GGAAGTGACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100  
GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150  
AGGAAGTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200  
GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250  
CAATGCTGCC CATTGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300

TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350  
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTAAAC AATGAGGTGA 2400  
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCCG CACGTGCC 2450  
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500  
 GAGGAAGAAC ATCAAGGGCA TCCATACCCCT CCTTCAGAAC TTGGCCAAGG 2550  
 CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600  
 GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTT 2650  
 AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATT 2700  
 ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750  
 TCCATAGACA CAGTATTGAC TTCTTTTGG CATTATCTCT TTCTCTCTT 2800  
 CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTAAATTTT CTTTTCTTC 2850  
 TTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCCTTC TTTGAATCA 2900  
 ATCTGGCTTC TGCATTACTA TTAACTCTGC ATAGACAAAG GCCTAACAA 2950  
 ACGTAATTG TTATATCAGC AGACACTCCA GTTGCCCCAC CACAACAAAC 3000  
 AATGCCTTGT TGTATTCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050  
 AAATATTTCA CTTAAACTTT GTCACTCTG CTGTACAGAT ATCGAGAGTT 3100  
 TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150  
 TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAAATC TAGA 3194

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 822 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10				15	
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
				20				25					30	

Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys  
                  35                        40                        45  
 Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro  
                  50                        55                        60  
 Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn  
                  65                        70                        75  
 Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr  
                  80                        85                        90  
 Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe  
                  95                        100                       105  
 Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile  
                  110                       115                       120  
 Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe  
                  125                       130                       135  
 Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe  
                  140                       145                       150  
 Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala  
                  155                       160                       165  
 Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser  
                  170                       175                       180  
 Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly  
                  185                       190                       195  
 Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu  
                  200                       205                       210  
 Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val  
                  215                       220                       225  
 Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met  
                  230                       235                       240  
 Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile  
                  245                       250                       255  
 Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn  
                  260                       265                       270  
 Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe  
                  275                       280                       285  
 Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His

290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu		
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile		
320	325	330
Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys		
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr		
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser		
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn		
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr		
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala		
425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met		
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys		
455	460	465
Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro		
470	475	480
Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu		
485	490	495
Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val		
500	505	510
Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys		
515	520	525
Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu		
530	535	540
Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala		
545	550	555

Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala  
 560 565 570  
 Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe  
 575 580 585  
 His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile  
 590 595 600  
 Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile Met  
 605 610 615  
 Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg  
 620 625 630  
 Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro  
 635 640 645  
 Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile  
 650 655 660  
 Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg  
 665 670 675  
 Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val  
 680 685 690  
 Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp  
 695 700 705  
 Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met  
 710 715 720  
 Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp  
 725 730 735  
 Val Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly  
 740 745 750  
 Lys Gln Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys  
 755 760 765  
 Ile Thr Gln Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln  
 770 775 780  
 Glu Val Tyr Glu Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His  
 785 790 795  
 Met Arg Lys Asn Ile Lys Gly Ile His Thr Leu Leu Gln Asn Leu  
 800 805 810

Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly  
 815                           820

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1870 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAAC CGCAAAGCGC AGGGAAAGGCC TCCCGGCACG 50  
 GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100  
 CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150  
 CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200  
 TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250  
 CGACCCTTCT CCTGGCATCG TGGCATTCC GAGATTGGAG CCTAACAGTG 300  
 TAGATCCTGA GAACATCACCC GAAATTTCA TCGCAAACCA GAAAAGGTTA 350  
 GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400  
 GACAATTGTG GATTCTGGAT TAAAATTGT GGCTCATAAA GCATTTCTGA 450  
 AAAACAGCAA CCTGCAGCAC ATCAATTTCG CCGAAACAA ACTGACGAGT 500  
 TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550  
 GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600  
 AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650  
 AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATAACCA ATTGTGGTTT 700  
 GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750  
 CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800  
 TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850  
 ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900  
 AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950

AACCTCACTG TGCATTTGC ACCAACTATC ACATTCTCG AATCTCCAAC 1000  
 CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050  
 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100  
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150  
 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200  
 CCAAGAATGA GTATGGGAAG GATGAGAAC AGATTTCTGC TCACTTCATG 1250  
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300  
 TTATGAAGAT TATGGAACTG CAGCGAATGA CATCGGGGAC ACCACGAACA 1350  
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400  
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTG 1450  
 CCTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTG 1500  
 GCATGAAAGG TTTTGTGTTG TTTCATAAGA TCCCAGTGGA TGGGTAGCTG 1550  
 AAATAAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600  
 TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGGAAGT 1650  
 GCTGCTTATC TGGGGTTTTC TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700  
 ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750  
 CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800  
 TTAATGCTTC TCTTCTTACA GTAGTTCAA TACAAAATG AAATGAAATC 1850  
 CCATTGGATT GTACTTCTCT 1870

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 477 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1														15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
														30
					20				25					

Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys  
                   35                  40                  45

Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro  
                   50                  55                  60

Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn  
                   65                  70                  75

Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr  
                   80                  85                  90

Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe  
                   95                  100                105

Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile  
                   110                115                120

Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe  
                   125                130                135

Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe  
                   140                145                150

Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala  
                   155                160                165

Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser  
                   170                175                180

Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly  
                   185                190                195

Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu  
                   200                205                210

Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val  
                   215                220                225

Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met  
                   230                235                240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile  
                   245                250                255

Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn  
                   260                265                270

Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe  
                   275                280                285

Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His  
 290 295 300  
 Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu  
 305 310 315  
 Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile  
 320 325 330  
 Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys  
 335 340 345  
 Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr  
 350 355 360  
 Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser  
 365 370 375  
 Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro  
 380 385 390  
 Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn  
 395 400 405  
 Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr  
 410 415 420  
 Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala  
 425 430 435  
 Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met  
 440 445 450  
 Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys  
 455 460 465  
 Gly Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly  
 470 475

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2715 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCCAGCCA AGTGTAGTTT 50

CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
CGCCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
ATATCACTTC CATAACACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300  
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400  
TGCCTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450  
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTT 500  
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550  
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600  
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650  
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700  
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750  
ACTGGGCTGC AGTCCATCAA CACTCACCAAG ACCAATCTGA ACTGGACCAA 800  
TGTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850  
GCTTCACCCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900  
AGTGTGCCC TCACTGTCTA CTATCCCCA CGTGTGGTGA GCCTGGAGGA 950  
GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTGTGGTG CGTGGCAACC 1000  
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050  
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATT CCGAGGGCTG 1100  
CCTGCTCTTC ACAAGGCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150  
TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200  
CTCAAGGAGC CCTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250  
AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300  
CTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTGC CTGTGTCTG 1350

TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400  
TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450  
GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500  
GCCGGGCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550  
GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CGGGACACGT 1600  
ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650  
GAGGGAGCCT TTGGAAAGGT CTTCTGGCC GAGTGCTACA ACCTCAGCCC 1700  
GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750  
TGGCTGCCCG GAAGGATTTC CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800  
CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGGCG ATGGGGACCC 1850  
CCTCATCATG GTCTTGAAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900  
TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950  
CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000  
GATGCCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050  
ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100  
GGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150  
CTTAATCCA TCTGGAAATG ATTTTGAT ATGGTGTGAG GTGGGAGGAC 2200  
ACACCATGCT CCCCATTGCG TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250  
AAGTCACTA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300  
GATTTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350  
TCATTGAGTG CATTACCAA GGTCGTGTT TGAGCGGCC CCGAGTCTGC 2400  
CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACACCA 2450  
GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGA 2500  
AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550  
ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600  
CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650

CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 839 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5					10					15
Phe Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu														
				20				25						30
Ala Cys Pro Ala Asn Cys Val Cys Ser Lys Thr Glu Ile Asn Cys														
				35			40							45
Arg Arg Pro Asp Asp Gly Asn Leu Phe Pro Leu Leu Glu Gly Gln														
				50			55							60
Asp Ser Gly Asn Ser Asn Gly Asn Ala Asn Ile Asn Ile Thr Asp														
				65			70							75
Ile Ser Arg Asn Ile Thr Ser Ile His Ile Glu Asn Trp Arg Ser														
				80			85							90
Leu His Thr Leu Asn Ala Val Asp Met Glu Leu Tyr Thr Gly Leu														
				95			100							105
Gln Lys Leu Thr Ile Lys Asn Ser Gly Leu Arg Ser Ile Gln Pro														
				110			115							120
Arg Ala Phe Ala Lys Asn Pro His Leu Arg Tyr Ile Asn Leu Ser														
				125			130							135
Ser Asn Arg Leu Thr Thr Leu Ser Trp Gln Leu Phe Gln Thr Leu														
				140			145							150
Ser Leu Arg Glu Leu Gln Leu Glu Gln Asn Phe Phe Asn Cys Ser														
				155			160							165
Cys Asp Ile Arg Trp Met Gln Leu Trp Gln Glu Gln Gly Glu Ala														
				170			175							180
Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala Asp Gly Ser														
				185			190							195

Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp Leu Pro  
 200 205 210

Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly Asp  
 215 220 225

Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp  
 230 235 240

Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln  
 245 250 255

Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu  
 260 265 270

Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile  
 275 280 285

Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr  
 290 295 300

Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu  
 305 310 315

Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro  
 320 325 330

Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser  
 335 340 345

Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu  
 350 355 360

Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn  
 365 370 375

Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr  
 380 385 390

Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp  
 395 400 405

Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr  
 410 415 420

Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala  
 425 430 435

Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe  
 440 445 450

Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys

455	460	465
Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro		
470	475	480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp		
485	490	495
Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val		
500	505	510
Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys		
515	520	525
Pro Asp Thr Tyr Val Gln His Ile Lys Arg Arg Asp Ile Val Leu		
530	535	540
Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala		
545	550	555
Glu Cys Tyr Asn Leu Ser Pro Thr Lys Asp Lys Met Leu Val Ala		
560	565	570
Val Lys Ala Leu Lys Asp Pro Thr Leu Ala Ala Arg Lys Asp Phe		
575	580	585
Gln Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile		
590	595	600
Val Lys Phe Tyr Gly Val Cys Gly Asp Gly Asp Pro Leu Ile Met		
605	610	615
Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg		
620	625	630
Ala His Gly Pro Asp Ala Met Ile Leu Val Asp Gly Gln Pro Arg		
635	640	645
Gln Ala Lys Gly Glu Leu Gly Leu Ser Gln Met Leu His Ile Ala		
650	655	660
Ser Gln Ile Ala Ser Gly Met Val Tyr Leu Ala Ser Gln His Phe		
665	670	675
Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Ala Asn		
680	685	690
Leu Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr		
695	700	705
Ser Thr Asp Tyr Tyr Arg Leu Phe Asn Pro Ser Gly Asn Asp Phe		
710	715	720

Cys Ile Trp Cys Glu Val Gly Gly His Thr Met Leu Pro Ile Arg  
 725 730 735

Trp Met Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu  
 740 745 750

Ser Asp Val Trp Ser Phe Gly Val Ile Leu Trp Glu Ile Phe Thr  
 755 760 765

Tyr Gly Lys Gln Pro Trp Phe Gln Leu Ser Asn Thr Glu Val Ile  
 770 775 780

Glu Cys Ile Thr Gln Gly Arg Val Leu Glu Arg Pro Arg Val Cys  
 785 790 795

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu  
 800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His  
 815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly  
 830 835

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1858 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50  
 CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100  
 TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150  
 CGGCGGCCGG ACGATGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200  
 AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250  
 ATATCACTTC CATAACACATA GAGAACTGGC GCAGTCTTCA CACGCTAAC 300  
 GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350  
 CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400

TGC GTT ATAT AAC CTC GTCA AGTA ACC CGGC TCACC AACT CTC GTGG CAG 450  
CTCT TCC AGA CGCT GAG TCT TCGGG AATTG CAG TTGG GAGC AGAA ACT TTTT 500  
CAACT GCAGC TGT GAC ATCC GCT GGAT GCA GCT CTGG CAG GAGC AGGGGG 550  
AGGCCAAGCT CAAC AGCCAG AAC CTCT ACT GCAT CAAT GC TGAT GGCT CC 600  
CAG CTT CCTC TCT TCC CGCAT GAAC ATCA GT CAGT GTG ACC TTC CTG AGAT 650  
CAG CGT GAGC CAC GTCA ACC TGAC CGT AC G AGAG GTG AC AAT GCT GTTA 700  
TCAC TTG CAA TGG CTCT GGA TCAC CCCT TC CTG AT GTG GA CTGG ATAG TC 750  
ACT GGG CTGC AGT CCAT CAA CACT CACC AG ACCA ATCT GA ACT GGAC CAA 800  
TGTT CATGCC ATCA ACTT GA CGCT GGT GAA TGT GAC GAGT GAGG ACA ATG 850  
GCTT CAC CCT GAC GTG CATT GCAG AGA AC G TG GTGG C AT GAG CA ATG CC 900  
AGT GTT GCCC TCA CT GTCT TA CT AT CCCC CA CGT GTGG TGA GC CTGG AGGA 950  
GC CTG AGCT G CGC CTGG AGC ACT GCAT CGA GT TT GTGG TG CGT GGCA ACC 1000  
CCCC ACCA AC GCT GCA CT GG CTG CACA ATG GG CAG C CT GC GGG AGT CC 1050  
AAG ATC ATCC AT GTG GAATA CT ACCA AGAG GG AGAG AT TT CCG AGGG CTG 1100  
CCT GCT CTTC AAC AAG CCCA CCC ACT ACAA CA AT GGCA AC TAT ACC CTCA 1150  
TTGCC AAAA CCC ACTGGC ACAG CCA ACC AG ACC ATCAA TGG CC ACTTC 1200  
CTCA AGG AGC CCT TTCC AGA GAG CAC GGG AT AACT TTAT CT TG TTG AC GA 1250  
AGT GAGT CCC ACAC CCT CTA TCA CT GTG AC CCAC AA ACCA GA AGA AGA CAA 1300  
CTTT TGGG GT ATCC ATAG CA GTT GGACT TG CTG CTTT GC CT GTG C CTG 1350  
TTGGTGGT TC TCT CGT CAT GAT CAAC AAA TAT GGTC GAC GGT CCA AATT 1400  
TGG AAT GAAG GGT CCC GT GG CT GT CAT CAG TG GTG AGG AG GACT CAG CCA 1450  
GCC CACT GCA CCAC ATCA AC CACGG CATCA CCAC GGC CTC GTC ACT GGAT 1500  
GCC GGG CCG AC ACT GT GG CATT GG CATG ACT CGC ATCC CT GT CATT GA 1550  
GAAC CCCC AG TACT CC GT C AGGG ACAC AA CTG CCAC AAG CGG ACAC GT 1600  
GGG TCTT TC AA ACAT AGAC AAT CATGG A TATT AA ACTT GA AGG AC AAT 1650  
AGAG ATC ATC TAGT CCC ATC AACT CACT AT AT ATG AGG AAC CTG AGG T 1700

CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750  
 TGTTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800  
 ATCTATGTTG AGGATGTCAA TGTGTTATTTC AGCAAAGGAC GTCATGGCCT 1850  
 TTAAAAAC 1858

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 612 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10					15	
Phe Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu														
		20				25							30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
				35				40					45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln
			50				55						60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp
			65				70						75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser
			80				85						90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu
			95					100					105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro
			110					115					120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser
			125				130						135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu
			140				145						150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser
			155				160						165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala
			170				175						180	

Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala Asp Gly Ser  
                  185                         190                         195

Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp Leu Pro  
                  200                         205                         210

Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly Asp  
                  215                         220                         225

Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp  
                  230                         235                         240

Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln  
                  245                         250                         255

Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu  
                  260                         265                         270

Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile  
                  275                         280                         285

Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr  
                  290                         295                         300

Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu  
                  305                         310                         315

Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro  
                  320                         325                         330

Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser  
                  335                         340                         345

Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu  
                  350                         355                         360

Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn  
                  365                         370                         375

Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr  
                  380                         385                         390

Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp  
                  395                         400                         405

Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr  
                  410                         415                         420

Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala  
                  425                         430                         435

Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe  
                   440  445  450  
  
 Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys  
                   455  460  465  
  
 Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro  
                   470  475  480  
  
 Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp  
                   485  490  495  
  
 Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val  
                   500  505  510  
  
 Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys  
                   515  520  525  
  
 Pro Asp Thr Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu  
                   530  535  540  
  
 Asn Leu Lys Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr  
                   545  550  555  
  
 Ile Tyr Glu Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro  
                   560  565  570  
  
 Arg Ser His Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu  
                   575  580  585  
  
 Pro Gly His Ser Lys Pro Leu Asn His Gly Ile Tyr Val Glu Asp  
                   590  595  600  
  
 Val Asn Val Tyr Phe Ser Lys Gly Arg His Gly Phe  
                   605  610

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 790 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu Arg Gly Gly Arg Arg Gly Gln Leu Gly Trp His Ser Trp  
                   1  5  10  15  
  
 Ala Ala Gly Pro Gly Ser Leu Leu Ala Trp Leu Ile Leu Ala Ser  
                   20  25  30  
  
 Ala Gly Ala Ala Pro Cys Pro Asp Ala Cys Cys Pro His Gly Ser

35	40	45
Ser Gly Leu Arg Cys	Thr Arg Asp Gly	Ala Leu Asp Ser Leu His
50	55	60
His Leu Pro Gly Ala	Glu Asn Leu Thr Glu	Leu Tyr Ile Glu Asn
65	70	75
Gln Gln His Leu Gln	His Leu Glu Leu Arg Asp	Leu Arg Gly Leu
80	85	90
Gly Glu Leu Arg Asn	Leu Thr Ile Val Lys	Ser Gly Leu Arg Phe
95	100	105
Val Ala Pro Asp Ala	Phe His Phe Thr	Pro Arg Leu Ser Arg
110	115	120
Asn Leu Ser Phe Asn	Ala Leu Glu Ser	Leu Ser Trp Lys Thr
125	130	135
Gln Gly Leu Ser	Leu Gln Glu Leu Val	Leu Ser Gly Asn Pro
140	145	150
His Cys Ser Cys Ala	Leu Arg Trp Leu Gln	Arg Trp Glu Glu
155	160	165
Gly Leu Gly Gly Val	Pro Glu Gln Lys	Leu Gln Cys His Gly
170	175	180
Gly Pro Leu Ala His	Met Pro Asn Ala	Ser Cys Gly Val Pro
185	190	195
Leu Lys Val Gln Val	Pro Asn Ala Ser	Val Asp Val Gly Asp
200	205	210
Val Leu Leu Arg Cys	Gln Val Glu Gly	Arg Gly Leu Glu Gln
215	220	225
Gly Trp Ile Leu Thr	Glu Leu Glu Gln	Ser Ala Thr Val Met
230	235	240
Ser Gly Gly Leu Pro	Ser Leu Gly Leu	Thr Leu Ala Asn Val
245	250	255
Ser Asp Leu Asn Arg	Lys Asn Leu Thr	Cys Trp Ala Glu Asn
260	265	270
Val Gly Arg Ala Glu	Val Ser Val Gln	Val Asn Val Ser Phe
275	280	285
Ala Ser Val Gln Leu	His Thr Ala Val	Glu Met His His Trp
290	295	300

CSEQLIST

Ile	Pro	Phe	Ser	Val	Asp	Gly	Gln	Pro	Ala	Pro	Ser	Leu	Arg	Trp
305								310					315	
Leu	Phe	Asn	Gly	Ser	Val	Leu	Asn	Glu	Thr	Ser	Phe	Ile	Phe	Thr
320								325					330	
Glu	Phe	Leu	Glu	Pro	Ala	Ala	Asn	Glu	Thr	Val	Arg	His	Gly	Cys
335								340					345	
Leu	Arg	Leu	Asn	Gln	Pro	Thr	His	Val	Asn	Asn	Gly	Asn	Tyr	Thr
350								355					360	
Leu	Leu	Ala	Ala	Asn	Pro	Phe	Gly	Gln	Ala	Ser	Ala	Ser	Ile	Met
365								370					375	
Ala	Ala	Phe	Met	Asp	Asn	Pro	Phe	Glu	Phe	Asn	Pro	Glu	Asp	Pro
380								385					390	
Ile	Pro	Asp	Thr	Asn	Ser	Thr	Ser	Gly	Asp	Pro	Val	Glu	Lys	Lys
395								400					405	
Asp	Glu	Thr	Pro	Phe	Gly	Val	Ser	Val	Ala	Val	Gly	Leu	Ala	Val
410								415					420	
Phe	Ala	Cys	Leu	Phe	Leu	Ser	Thr	Leu	Leu	Leu	Val	Leu	Asn	Lys
425								430					435	
Cys	Gly	Arg	Arg	Asn	Lys	Phe	Gly	Ile	Asn	Arg	Pro	Ala	Val	Leu
440								445					450	
Ala	Pro	Glu	Asp	Gly	Leu	Ala	Met	Ser	Leu	His	Phe	Met	Thr	Leu
455								460					465	
Gly	Gly	Ser	Ser	Leu	Ser	Pro	Thr	Glu	Gly	Lys	Gly	Ser	Gly	Leu
470								475					480	
Gln	Gly	His	Ile	Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Ser	Asp	Ala	Cys
485								490					495	
Val	His	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu	Lys	Trp	Glu	Leu
500								505					510	
Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	His	Asn
515								520					525	
Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu
530								535					540	
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala
545								550					555	

Glu Leu Leu Thr Met Leu Gln His Gln His Ile Val Arg Phe Phe  
 560 565 570

Gly Val Cys Thr Glu Gly Arg Pro Leu Leu Met Val Phe Glu Tyr  
 575 580 585

Met Arg His Gly Asp Leu Asn Arg Phe Leu Arg Ser His Gly Pro  
 590 595 600

Asp Ala Lys Leu Leu Ala Gly Gly Glu Asp Val Ala Pro Gly Pro  
 605 610 615

Leu Gly Leu Gly Gln Leu Leu Ala Val Ala Ser Gln Val Ala Ala  
 620 625 630

Gly Met Val Tyr Leu Ala Gly Leu His Phe Val His Arg Asp Leu  
 635 640 645

Ala Thr Arg Asn Cys Leu Val Gly Gln Gly Leu Val Val Lys Ile  
 650 655 660

Gly Asp Phe Gly Met Ser Arg Asp Ile Tyr Ser Thr Asp Tyr Tyr  
 665 670 675

Arg Val Gly Gly Arg Thr Met Leu Pro Ile Arg Trp Met Pro Pro  
 680 685 690

Glu Ser Ile Leu Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp  
 695 700 705

Ser Phe Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln  
 710 715 720

Pro Trp Tyr Gln Leu Ser Asn Thr Glu Ala Ile Asp Cys Ile Thr  
 725 730 735

Gln Gly Arg Glu Leu Glu Arg Pro Arg Ala Cys Pro Pro Glu Val  
 740 745 750

Tyr Ala Ile Met Arg Gly Cys Trp Gln Arg Glu Pro Gln Gln Arg  
 755 760 765

His Ser Ile Lys Asp Val His Ala Arg Leu Gln Ala Leu Ala Gln  
 770 775 780

Ala Pro Pro Val Tyr Leu Asp Val Leu Gly  
 785 790

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAA RAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYTTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGR RTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu Asn Leu Lys  
1 5 10 15

Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr Ile Tyr Glu  
20 25 30

Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro Arg Ser His  
35 40 45

Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu Pro Gly His  
50 55 60

## GENENT.33CPC4Cseqlist.txt

Ser Lys Pro Leu Asn His Gly Ile Tyr Val Glu Asp Val Asn Val  
65 70 75

Tyr Phe Ser Lys Gly Arg His Gly Phe  
80